

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 09/522,753 C
Source: IFW/b
Date Processed by STIC: 5/30/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 06/02/2006

PATENT APPLICATION: US/09/522,753C

TIME: 15:51:32

Input Set : A:\SALK1510.APP

Output Set: N:\CRF4\06022006\I522753C.raw

3 <110> APPLICANT: EVANS, RONALD M.
 4 CHEN, J. DON
 5 ORDENTLICH, PETER
 6 DOWNES, MICHAEL R.
 8 <120> TITLE OF INVENTION: FAMILY OF TRANSCRIPTIONAL CO-REPRESSORS THAT INTERACT
 9 WITH NUCLEAR HORMONE RECEPTORS AND USES THEREFOR
 11 <130> FILE REFERENCE: SALK1510-3
 13 <140> CURRENT APPLICATION NUMBER: 09/522,753C
 14 <141> CURRENT FILING DATE: 2000-03-10
 16 <150> PRIOR APPLICATION NUMBER: 08/522,726
 17 <151> PRIOR FILING DATE: 1995-09-01
 19 <160> NUMBER OF SEQ ID NOS: 52
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1495
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
 29 Met Glu Ala Trp Asp Ala His Pro Asp Lys Glu Ala Phe Ala Ala Glu
 30 1 5 10 15
 32 Ala Gln Lys Leu Pro Gly Asp Pro Pro Cys Trp Thr Ser Gly Leu Pro
 33 20 25 30
 35 Phe Pro Val Pro Pro Arg Glu Val Ile Lys Ala Ser Pro His Ala Pro
 36 35 40 45
 38 Asp Pro Ser Ala Phe Ser Tyr Ala Pro Pro Gly His Pro Leu Pro Leu
 39 50 55 60
 41 Gly Leu His Asp Thr Ala Arg Pro Val Leu Pro Arg Pro Pro Thr Ile
 42 65 70 75 80
 44 Ser Asn Pro Pro Pro Leu Ile Ser Ser Ala Lys His Pro Ser Val Leu
 45 85 90 95
 47 Glu Arg Gln Ile Gly Ala Ile Ser Gln Gly Met Ser Val Gln Leu His
 48 100 105 110
 50 Val Pro Tyr Ser Glu His Ala Lys Ala Pro Val Gly Pro Val Thr Met
 51 115 120 125
 53 Gly Leu Pro Leu Pro Met Asp Pro Lys Lys Leu Ala Pro Phe Ser Gly
 54 130 135 140
 56 Val Lys Gln Glu Gln Leu Ser Pro Arg Gly Gln Ala Gly Pro Pro Glu
 57 145 150 155 160
 59 Ser Leu Gly Val Pro Thr Ala Gln Glu Ala Ser Val Leu Arg Gly Thr
 60 165 170 175
 62 Ala Leu Gly Ser Val Pro Gly Gly Ser Ile Thr Lys Gly Ile Pro Ser
 63 180 185 190
 65 Thr Arg Val Pro Ser Asp Ser Ala Ile Thr Tyr Arg Gly Ser Ile Thr

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66          195          200          205
68 His Gly Thr Pro Ala Asp Val Leu Tyr Lys Gly Thr Ile Thr Arg Ile
69          210          215          220
71 Ile Gly Glu Asp Ser Pro Ser Arg Leu Asp Arg Gly Arg Glu Asp Ser
72 225          230          235          240
74 Leu Pro Lys Gly His Val Ile Tyr Glu Gly Lys Lys Gly His Val Leu
75          245          250          255
77 Ser Tyr Glu Gly Gly Met Ser Val Thr Gln Cys Ser Lys Glu Asp Gly
78          260          265          270
80 Arg Ser Ser Ser Gly Pro Pro His Glu Thr Ala Ala Pro Lys Arg Thr
81          275          280          285
83 Tyr Asp Met Met Glu Gly Arg Val Gly Arg Ala Ile Ser Ser Ala Ser
84          290          295          300
86 Ile Glu Gly Leu Met Gly Arg Ala Ile Pro Pro Glu Arg His Ser Pro
87 305          310          315          320
89 His His Leu Lys Glu Gln His His Ile Arg Gly Ser Ile Thr Gln Gly
90          325          330          335
92 Ile Pro Arg Ser Tyr Val Glu Ala Gln Glu Asp Tyr Leu Arg Arg Glu
93          340          345          350
95 Ala Lys Leu Leu Lys Arg Glu Gly Thr Pro Pro Pro Pro Pro Pro Ser
96          355          360          365
98 Arg Asp Leu Thr Glu Ala Tyr Lys Thr Gln Ala Leu Gly Pro Leu Lys
99          370          375          380
101 Leu Lys Pro Ala His Glu Gly Leu Val Ala Thr Val Lys Glu Ala Gly
102 385          390          395          400
104 Arg Ser Ile His Glu Ile Pro Arg Glu Glu Leu Arg His Thr Pro Glu
105          405          410          415
107 Leu Pro Leu Ala Pro Arg Pro Leu Lys Glu Gly Ser Ile Thr Gln Gly
108          420          425          430
110 Thr Pro Leu Lys Tyr Asp Thr Gly Ala Ser Thr Thr Gly Ser Lys Lys
111          435          440          445
113 His Asp Val Arg Ser Leu Ile Gly Ser Pro Gly Arg Thr Phe Pro Pro
114          450          455          460
116 Val His Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala
117 465          470          475          480
119 Cys Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser
120          485          490          495
122 Gly Gly Ser Ile Ala Arg Gly Ala Pro Val Ile Val Pro Glu Leu Gly
123          500          505          510
125 Lys Pro Arg Gln Ser Pro Leu Thr Tyr Glu Asp His Gly Ala Pro Phe
126          515          520          525
128 Ala Gly His Leu Pro Arg Gly Ser Pro Val Thr Met Arg Glu Pro Thr
129          530          535          540
131 Pro Arg Leu Gln Glu Gly Ser Leu Ser Ser Ser Lys Ala Ser Gln Asp
132 545          550          555          560
134 Arg Lys Leu Thr Ser Thr Pro Arg Glu Ile Ala Lys Ser Pro His Ser
135          565          570          575
137 Thr Val Pro Glu His His Pro His Pro Ile Ser Pro Tyr Glu His Leu
138          580          585          590

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```

140 Leu Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu
141      595      600      605
143 Ala Phe Asp Pro Thr Ser Ile Pro Arg Gly Ile Pro Leu Asp Ala Ala
144      610      615      620
146 Ala Ala Tyr Tyr Leu Pro Arg His Leu Ala Pro Asn Pro Thr Tyr Pro
147 625      630      635      640
149 His Leu Tyr Pro Pro Tyr Leu Ile Arg Gly Tyr Pro Asp Thr Ala Ala
150      645      650      655
152 Leu Glu Asn Arg Gln Thr Ile Ile Asn Asp Tyr Ile Thr Ser Gln Gln
153      660      665      670
155 Met His His Asn Thr Ala Thr Ala Met Ala Gln Arg Ala Asp Met Leu
156      675      680      685
158 Arg Gly Leu Ser Pro Arg Glu Ser Ser Leu Ala Leu Asn Tyr Ala Ala
159      690      695      700
161 Gly Pro Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val
162 705      710      715      720
164 Leu Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu
165      725      730      735
167 Ala Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser
168      740      745      750
170 Ser Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro Thr Thr
171      755      760      765
173 Thr Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg
174      770      775      780
176 Asp Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Thr Val Glu
177 785      790      795      800
179 His Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser
180      805      810      815
182 Gly Ser Ser Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His
183      820      825      830
185 Ser His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala
186      835      840      845
188 Leu Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile
189      850      855      860
191 Ile Thr Ala Val Glu Pro Ser Lys Pro Thr Val Leu Arg Ser Thr Ser
192 865      870      875      880
194 Thr Ser Ser Pro Val Arg Pro Ala Ala Thr Phe Pro Pro Ala Thr His
195      885      890      895
197 Cys Pro Leu Gly Gly Thr Leu Asp Gly Val Tyr Pro Thr Leu Met Glu
198      900      905      910
200 Pro Val Leu Leu Pro Lys Glu Ala Pro Arg Val Ala Arg Pro Glu Arg
201      915      920      925
203 Pro Arg Ala Asp Thr Gly His Ala Phe Leu Ala Lys Pro Pro Ala Arg
204      930      935      940
206 Ser Gly Leu Glu Pro Ala Ser Ser Pro Ser Lys Gly Ser Glu Pro Arg
207 945      950      955      960
209 Pro Leu Val Pro Pro Val Ser Gly His Ala Thr Ile Ala Arg Thr Pro
210      965      970      975
212 Ala Lys Asn Leu Ala Pro His His Ala Ser Pro Asp Pro Pro Ala Pro

```

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```

213          980          985          990
215 Pro Ala Ser Ala Ser Asp Pro His Arg Glu Lys Thr Gln Ser Lys Pro
216          995          1000          1005
218 Phe Ser Ile Gln Glu Leu Glu Leu Arg Ser Leu Gly Tyr His Gly Ser
219      1010          1015          1020
221 Ser Tyr Ser Pro Glu Gly Val Glu Pro Val Ser Pro Val Ser Ser Pro
222 1025          1030          1035          1040
224 Ser Leu Thr His Asp Lys Gly Leu Pro Lys His Leu Glu Glu Leu Asp
225          1045          1050          1055
227 Lys Ser His Leu Glu Gly Glu Leu Arg Pro Lys Gln Pro Gly Pro Val
228          1060          1065          1070
230 Lys Leu Gly Gly Glu Ala Ala His Leu Pro His Leu Arg Pro Leu Pro
231      1075          1080          1085
233 Glu Ser Gln Pro Ser Ser Ser Pro Leu Leu Gln Thr Ala Pro Gly Val
234      1090          1095          1100
236 Lys Gly His Gln Arg Val Val Thr Leu Ala Gln His Ile Ser Glu Val
237 1105          1110          1115          1120
239 Ile Thr Gln Asp Tyr Thr Arg His His Pro Gln Gln Leu Ser Ala Pro
240          1125          1130          1135
242 Leu Pro Ala Pro Leu Tyr Ser Phe Pro Gly Ala Ser Cys Pro Val Leu
243          1140          1145          1150
245 Asp Leu Arg Arg Pro Pro Ser Asp Leu Tyr Leu Pro Pro Pro Asp His
246          1155          1160          1165
248 Gly Ala Pro Ala Arg Gly Ser Pro His Ser Glu Gly Gly Lys Arg Ser
249      1170          1175          1180
251 Pro Glu Pro Asn Lys Thr Ser Val Leu Gly Gly Gly Glu Asp Gly Ile
252 1185          1190          1195          1200
254 Glu Pro Val Ser Pro Pro Glu Gly Met Thr Glu Pro Gly His Ser Arg
255          1205          1210          1215
257 Ser Ala Val Tyr Pro Leu Leu Tyr Arg Asp Gly Glu Gln Thr Glu Pro
258          1220          1225          1230
260 Ser Arg Met Gly Ser Lys Ser Pro Gly Asn Thr Ser Gln Pro Pro Ala
261      1235          1240          1245
263 Phe Phe Ser Lys Leu Thr Glu Ser Asn Ser Ala Met Val Lys Ser Lys
264      1250          1255          1260
266 Lys Gln Glu Ile Asn Lys Lys Leu Asn Thr His Asn Arg Asn Glu Pro
267 1265          1270          1275          1280
269 Glu Tyr Asn Ile Ser Gln Pro Gly Thr Glu Ile Phe Asn Met Pro Ala
270          1285          1290          1295
272 Ile Thr Gly Thr Gly Leu Met Thr Tyr Arg Ser Gln Ala Val Gln Glu
273          1300          1305          1310
275 His Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu
276      1315          1320          1325
278 Met Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn
279      1330          1335          1340
281 Ala Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro
282 1345          1350          1355          1360
284 Ile Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro Gly
285          1365          1370          1375

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```

287 Gly Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala
288           1380           1385           1390
290 Lys Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val
291           1395           1400           1405
293 Ser Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr
294           1410           1415           1420
296 Asn Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe
297 1425           1430           1435           1440
299 Pro Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser
300           1445           1450           1455
302 Pro Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro
303           1460           1465           1470
305 His His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr
306           1475           1480           1485
308 Glu Thr Leu Ser Asp Ser Glu
309           1490           1495

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312 <210> SEQ ID NO: 2

313 <211> LENGTH: 46

314 <212> TYPE: PRT

315 <213> ORGANISM: Homo sapiens

317 <400> SEQUENCE: 2

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318 His Ser Asp Val Ser Glu Ser Lys Arg Lys Arg Phe Glu Leu Asn Ser
319   1           5           10           15
321 Gly Glu Ala Gly Gly Asn Ala Thr Ser Ala Met Thr Asn Ser Ser Thr
322           20           25           30
324 Ser Gly Ser Met Asn Ile Ser Asn Ser His Gly Leu Lys Ala
325           35           40           45

```

328 <210> SEQ ID NO: 3

329 <211> LENGTH: 17

330 <212> TYPE: DNA

331 <213> ORGANISM: Saccharomyces sp.

333 <400> SEQUENCE: 3

334 cggaggactg tcctccg

17

337 <210> SEQ ID NO: 4

338 <211> LENGTH: 8561

339 <212> TYPE: DNA

340 <213> ORGANISM: Homo sapiens

342 <400> SEQUENCE: 4

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343 catgtcgggc tccacacagc ttgtggcaca gacgtggagg gccactgagc cccgctaccc 60
344 gccccacagc ctttcctacc cagtgcagat cgcccggacg cacacggacg tcgggctcct 120
345 ggagtaccag caccactccc gcgactatgc ctcccacctg tcgccgggct ccatcatcca 180
346 gccccagcgg cggaggccct cctgctgtc tgagttccag cccgggaatg aacggtccca 240
347 ggagctccac ctgcggccag agtcccactc atacctgccc gagctgggga agtcagagat 300
348 ggagttcatt gaaagcaagc gccctcggct agagctgctg cctgaccccc tgctgcgacc 360
349 gtcacccctg ctggccacgg gccagcctgc gggatctgaa gacctacca aggaccgtag 420
350 cctgacgggc aagctggaac cggtgtctcc cccagcccc cgcacactg accctgagct 480
351 ggagctgggt cgcgccaggg tgtccaagga ggagctgatc cagaacatgg accgcgtgga 540
352 ccgagagatc accatggtag agcagcagat ctctaagctg aagaagaagc agcaacagct 600
353 ggaggaggag gctgccaagc cgcccagacc tgagaagccc gtgtcaccgc cgcccatcga 660

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/02/2006
PATENT APPLICATION: US/09/522,753C TIME: 15:51:33

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Output Set: N:\CRF4\06022006\I522753C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 109,8173,8180,8302,8343,8359,8384

Seq#:8; N Pos. 7250,7257,7379,7420,7436,7461

VERIFICATION SUMMARY

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L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:60

M:341 Repeated in SeqNo=6

L:1780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:7200

M:341 Repeated in SeqNo=8